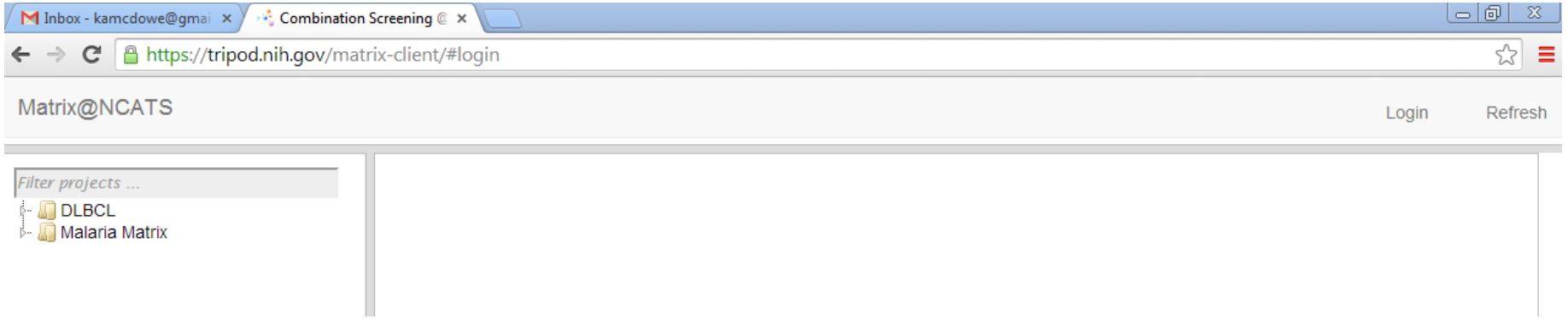
NCATS Tripod Site Tutorial

Tripod Site

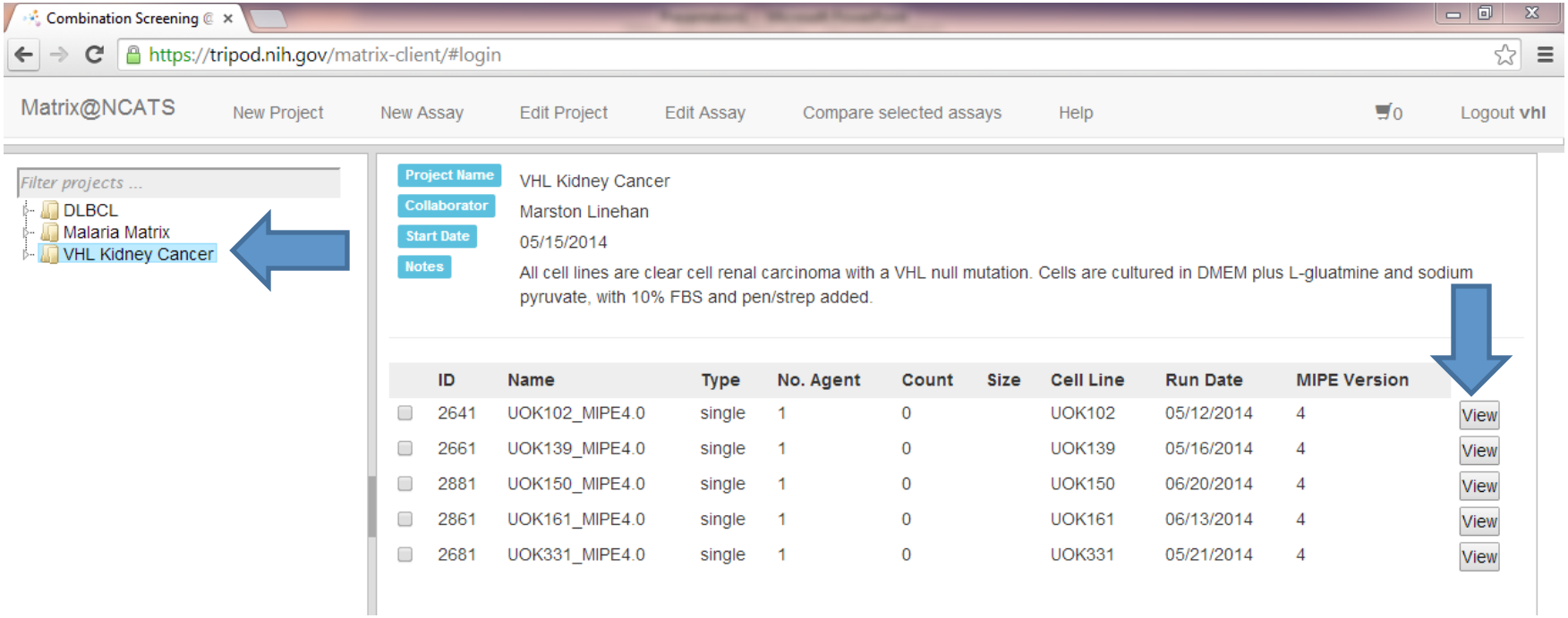


- Go to https://tripod.nih.gov/matrix-client/ using Chrome or Firefox. Do not use Internet Explorer!
- Click "Login" in top right corner
- Username and Password must be created by Raj
- Once you are logged in, folders you have access to will display in the left panel

Viewing and Downloading Data

1. Click on your Assay of interest in the left panel
2. Click the Heatmap Icon to view dose response curves (single agent screen) or matrix (combination screen)
3. Click the List Icon to view individual information for each compound or combination screened
4. Click the QC Diagnostics Icon for QC information on that assay

Viewing Data Online

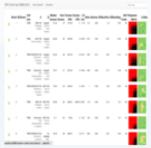


- Click on the VHL Kidney Cancer folder on the right panel
- Then click View on the far right

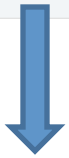
VHL Kidney Cancer / UOK102_MIPE4.0

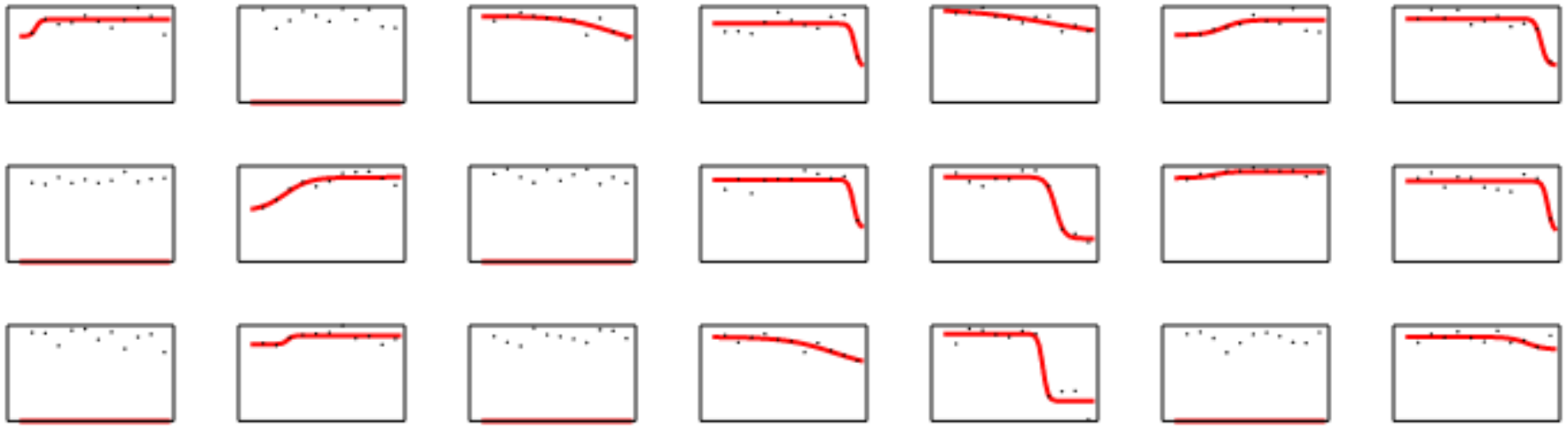
Collaborator	Marston Linehan
Start Date	05/15/2014
Notes	All cell lines are clear cell renal carcinoma with a VHL null mutation. Cells are cultured in DMEM plus L-gluatmine and sodium pyruvate, with 10% FBS and pen/strep added.

Assay ID	2641
Canonical Name	384_0x0_4_single_UOK102_Marston Linehan_Cell Titer Glow_48.0 hour
FOTS ID Type	single with MIPE v4
Num Component	1
Block Size qHTS protocol	s-vhl-UOK102-1
Assay Volume	5.0 uL
Readout	Cell Titer Glow at 48.0 hour
Run date	05/12/2014
Notes	UOK102 cells were plated at 500 cells per well then incubated for 4 hours. Next, compounds were added. Plates incubated with compound for 48 hours then Cell Titer Glo was added.



QC DIAGNOSTICS

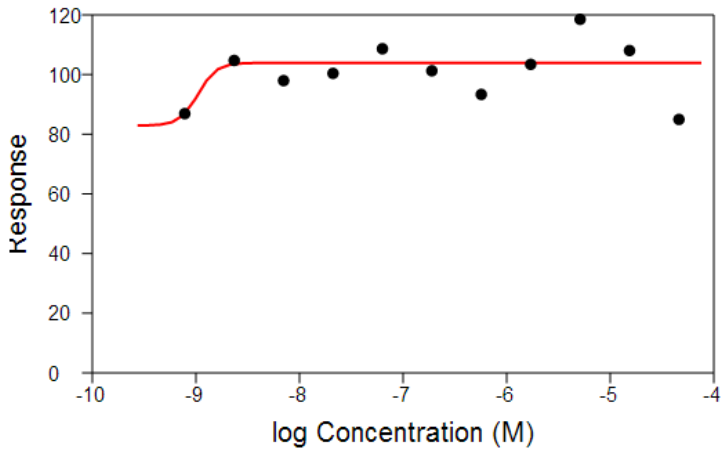




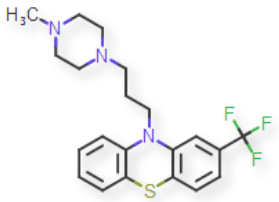
Serial	NCGC ID	Name	Target	MoA	AC50 (uM)	Hill Slope	Infinity	Zero	Curve Class[?]	Curve Class2[?]	Read
1	NCGC00013226-15	Trifluoperazine hydrochloride	DRD2	Nav1.4 (SkM1) Sodium Channel Blockers;Nav 1.7 (PN1/hNE-Na) Sodium Channel Blockers	0.00	4.95	103.90	82.90	1.3	1.4	ac ty

NCGC00013226-15 Trifluoperazine hydrochloride

activity



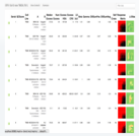
Curve class	1.3
Curve class 2	1.4
AC_{50}	0.00 uM
Hill slope	4.95
Zero Activity	82.90
Inf. Activity	103.90



NCGC ID	NCGC00013226-15
Name	Trifluoperazine hydrochloride
MoA	Nav1.4 (SkM1) Sodium Channel Blockers;Nav1.7 (PN1/hNE-Na) Sodium Channel Blockers
Aliases	Trifluoperazine dihydrochloride, Trifluoperazine Hcl, Stelabid, Stelazine, Stelazine trifluoperzine, Trifluoperazina
CAS RN	440-17-5
Alt. Mechanism	

VHL Kidney Cancer / UOK102_MIPE4.0

Collaborator	Marston Linehan
Start Date	05/15/2014
Notes	All cell lines are clear cell renal carcinoma with a VHL null mutation. Cells are cultured in DMEM plus L-gluatmine and sodium pyruvate, with 10% FBS and pen/strep added.
Assay ID	2641
Canonical Name	384_0x0_4_single_UOK102_Marston Linehan_Cell Titer Glow_48.0 hour
FOTS ID Type	single with MIPE v4
Num Component	1
Block Size qHTS protocol	s-vhl-UOK102-1
Assay Volume	5.0 uL
Readout	Cell Titer Glow at 48.0 hour
Run date	05/12/2014
Notes	UOK102 cells were plated at 500 cells per well then incubated for 4 hours. Next, compounds were added. Plates incubated with compound for 48 hours then Cell Titer Glo was added.



Only 10 compounds will display by default. To display everything, select all in the pull down menu then click the refresh button.

Download all data here!

1912 samples, 1 readout

Download data

Items to display 10

Highlight actives

← Previous

Next →

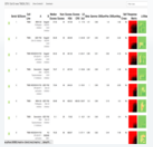
Clicking on any of the headings will sort all the data by that column

Serial	NCGC ID	Name	Target	MoA	AC50 (uM)	Hill Slope	Infinity	Zero	Curve Class?	Curve Class2?	Readout	
1	NCGC00013226-15	Trifluoperazine hydrochloride	DRD2	Nav1.4 (SkM1) Sodium Channel Blockers;Nav 1.7 (PN1/hNE-Na) Sodium Channel Blockers	0.00	4.95	103.90	82.90	1.3	1.4	activity	
2	NCGC00013724-01	Methscopolamine bromide		Muscarinic Antagonists	1000000.00	0.00	0.00	0.00	5	4	activity	

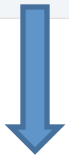
VHL Kidney Cancer / UOK102_MIPE4.0

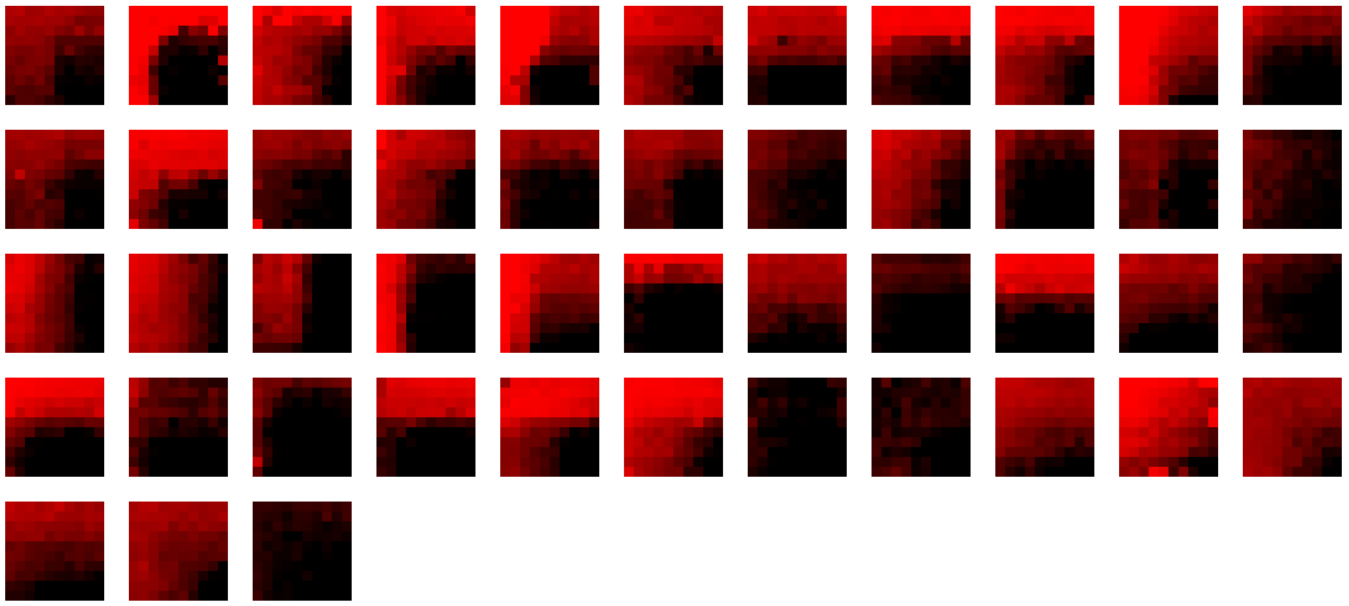
Collaborator	Marston Linehan
Start Date	05/15/2014
Notes	All cell lines are clear cell renal carcinoma with a VHL null mutation. Cells are cultured in DMEM plus L-gluatmine and sodium pyruvate, with 10% FBS and pen/strep added.

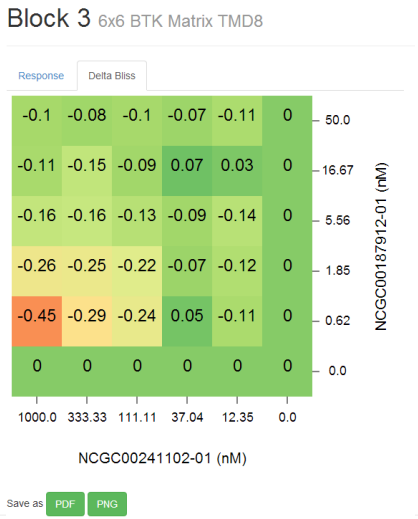
Assay ID	2641
Canonical Name	384_0x0_4_single_UOK102_Marston Linehan_Cell Titer Glow_48.0 hour
FOTS ID Type	single with MIPE v4
Num Component	1
Block Size qHTS protocol	s-vhl-UOK102-1
Assay Volume	5.0 uL
Readout	Cell Titer Glow at 48.0 hour
Run date	05/12/2014
Notes	UOK102 cells were plated at 500 cells per well then incubated for 4 hours. Next, compounds were added. Plates incubated with compound for 48 hours then Cell Titer Glo was added.



QC DIAGNOSTICS

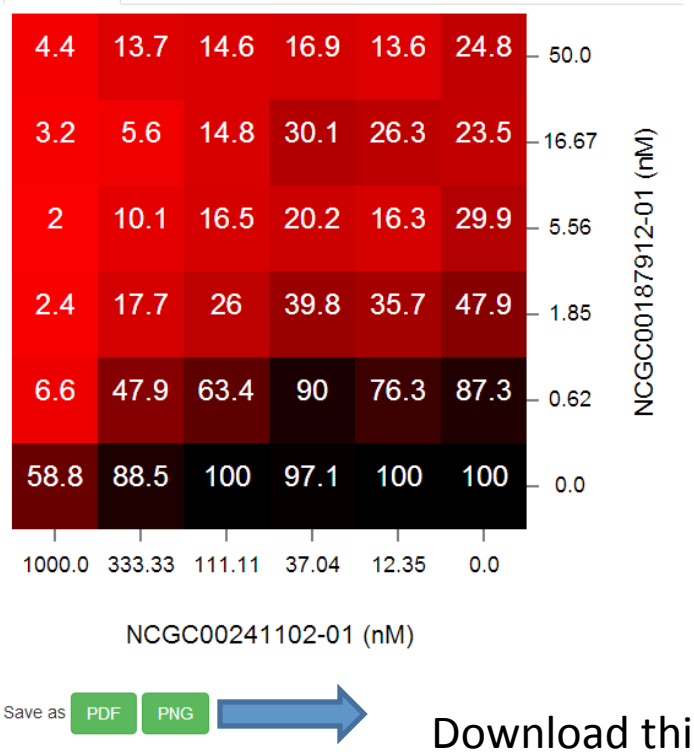


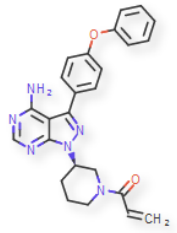




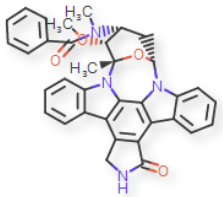
Red wells = viability readout, values are from CTG

Green wells = synergy assessment based on viability readout





NCGC ID	NCGC00187912-01
Name	PCI-32765
MoA	Btk/Lck/Lyn inhibitor
Aliases	PCI-32765
CAS RN	936563-96-1
Alt. Mechanism	
Phase	



NCGC ID	NCGC00241102-01
Name	Midostaurin
MoA	PKC/flt3 inhibitor
Aliases	Midostaurin, PKC 412, CGP-41251/PKC-412
CAS RN	120685-11-2
Alt. Mechanism	
Phase	

Download this specific matrix data

VHL Kidney Cancer / UOK102_MIPE4.0

Collaborator	Marston Linehan
Start Date	05/15/2014
Notes	All cell lines are clear cell renal carcinoma with a VHL null mutation. Cells are cultured in DMEM plus L-gluatmine and sodium pyruvate, with 10% FBS and pen/strep added.
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Assay Volume	5.0 uL
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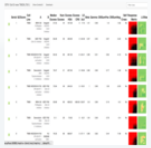
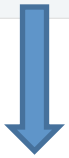
Run date	05/12/2014
Notes	UOK102 cells were plated at 500 cells per well then incubated for 4 hours. Next, compounds were added. Plates incubated with compound for 48 hours then Cell Titer Glo was added.





TMD8

https://tripod.nih.gov/matrix-client/rest/matrix/blocks/168/table

6x6 BTK Matrix TMD8 (168) Show ComboID Selection Download 0 Filter rows

	Serial	QCScore	Cell Line	A	B	Median Excess	Num Excess	Excess HSA	Excess CRX	LS 3x3	Beta	Gamma	DBSumPos	DBSumNeg	Self Cross	Response Matrix	Δ Bliss
	1		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Canertinib *EGFR (HER1; erbB1) inhibitor*	84.21	6	581.06	581.06	11.74	1.19	1.18	6.67	-0.55	No		
	2		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Neratinib *EGFR (HER1; erbB1) inhibitor*	78.45	18	-207.68	-207.68	-14.72	0.93	0.91	0.38	-1.86	No		
	3		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Midostaurin *PKC/flt3 inhibitor*	91.03	22	-424.84	-424.84	-27.91	0.87	0.83	0.15	-3.5	No		
	4		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	TAE-684 *Anaplastic Lymphoma Kinase (ALK) Inhibitor*	86.5	24	-282.82	-282.82	-13.49	0.9	0.89	0.03	-2.67	No		
	5		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	AZD-7762 *Chk1/2 Inhibitor*	90.19	14	-205.84	0	-17.56	0.9	0.85	0.17	-1.69	No		

TMD8

https://tripod.nih.gov/matrix-client/rest/matrix/blocks/168/table

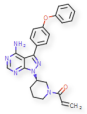
6x6 BTK Matrix TMD8 (168) Show ComboID Selection Download 0 Filter rows

	Serial	QCScore	Cell Line	A	B	Median Excess	Num Excess	Excess HSA	Excess CRX	LS 3x3	Beta	Gamma	DBSumPos	DBSumNeg	Self Cross	Response Matrix	Δ Bliss
	1		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Canertinib *EGFR (HER1; erbB1) inhibitor*	84.21	6	581.06	581.06	11.74	1.19	1.18	6.67	-0.55	No		
	2		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Neratinib *EGFR (HER1; erbB1) inhibitor*	78.45	18	-207.68	-207.68	-14.72	0.93	0.91	0.38	-1.86	No		
	3		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Midostaurin *PKC/flt3 inhibitor*	91.03	22	-424.84	-424.84	-27.91	0.87	0.83	0.15	-3.5	No		
	4		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	TAE-684 *Anaplastic Lymphoma Kinase (ALK) Inhibitor*	86.5	24	-282.82	-282.82	-13.49	0.9	0.89	0.03	-2.67	No		
	5		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	AZD-7762 *Chk1/2 Inhibitor*	90.19	14	-205.84	0	-17.56	0.9	0.85	0.17	-1.69	No		

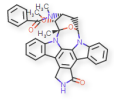
Block 3 6x6 BTK Matrix TMD8

Response Delta Bliss

NCGC00187912-01 (nM) \ NCGC00241102-01 (nM)	1000.0	333.33	111.11	37.04	12.35	0.0
50.0	4.4	13.7	14.6	16.9	13.6	24.8
16.67	3.2	5.6	14.8	30.1	26.3	23.5
5.56	2	10.1	16.5	20.2	16.3	29.9
1.85	2.4	17.7	26	39.8	35.7	47.9
0.62	6.6	47.9	63.4	90	76.3	87.3
0.0	58.8	88.5	100	97.1	100	100

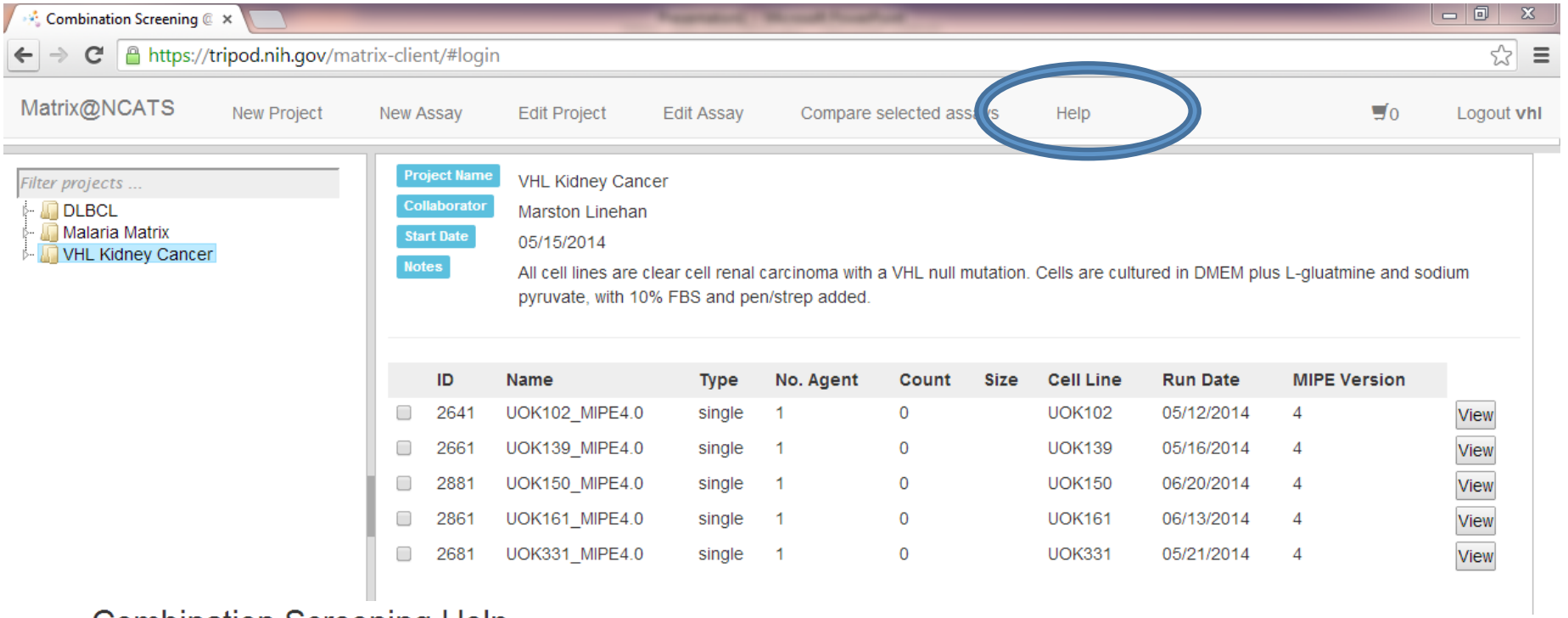


NCGC ID	NCGC00187912-01
Name	PCI-32765
MoA	Btk/Lck/Lyn inhibitor
Aliases	PCI-32765
CAS RN	936563-96-1
Alt. Mechanism	
Phase	



NCGC ID	NCGC00241102-01
Name	Midostaurin
MoA	PKC/flt3 inhibitor
Aliases	Midostaurin, PKC 412, CGP-41251/PKC-412
CAS RN	120685-11-2
Alt. Mechanism	
Phase	

Save as PDF PNG



Combination Screening Help

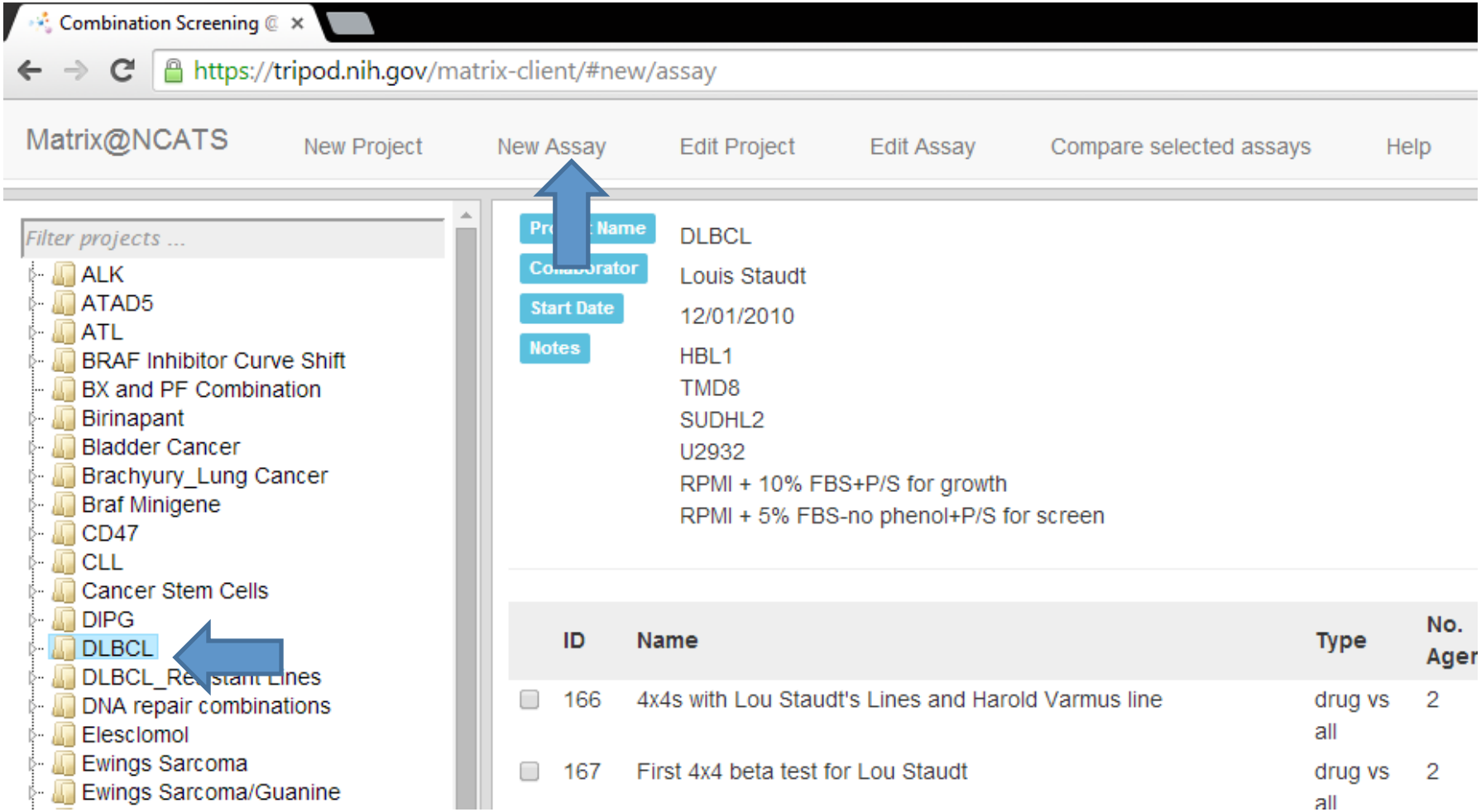
The *Tabular* tab summarizes the results of a combination screen. Several metrics of synergy are reported and their details are provided below. Our experience has shown that no single metric is effective in characterizing synergy over a large number of cases and that correlation between some of these metrics are relatively poor.

Clicking on NCGC ID's (columns **A** and **B**) will display an information box for the compounds. Clicking on the heatmaps will display a larger version of the heatmap along with the information boxes of the two compounds for that combination. Clicking on column headers will allow you to sort the entire table by that column.

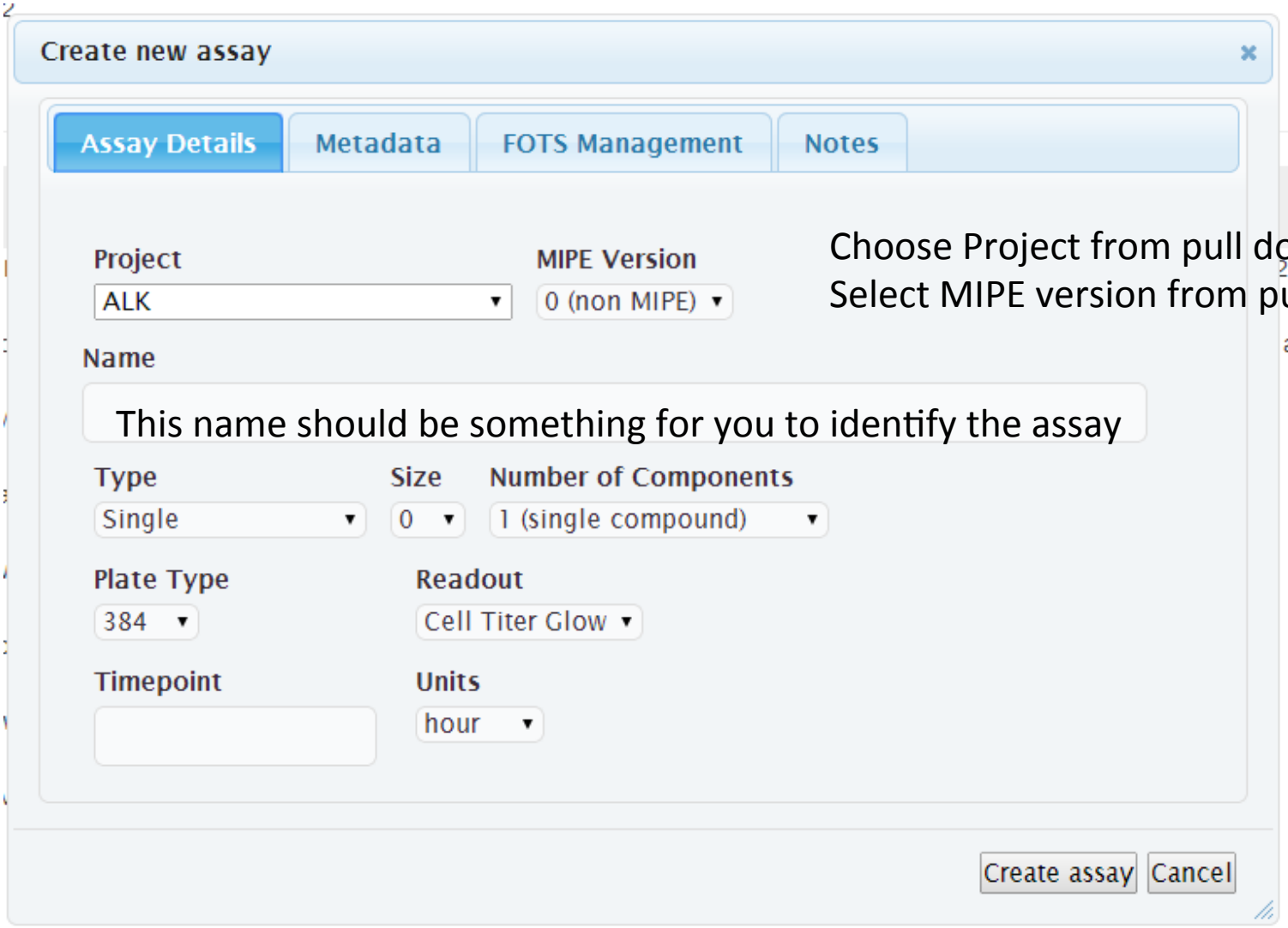
- **MedianExcess**: The median of the sum of the differences between the combination responses and the single agent responses. More positive values are better
- **NumExcess**: The number of combinations in a block that show a better combination responses than *both* the corresponding single agents. Larger is better
- **Excess HSA**: The HSA (see below) model is computed and the differences between each combination in the block and the corresponding HSA value are summed. More negative values are better
- **ExcessCRX**: An extension of the 'Excess HSA' metric that takes into account dilution factors. These factors are based on the EC_{90} and EC_{10} values of the single agent curves. Since the single agent curves are derived from the individual blocks, they can be noisy and thus the EC_{90} and EC_{10} can be inaccurate, resulting in noisy values for this metric. See Lehar et al for more information
- **LS 3x3**: The sum of the deviations from the HSA model are evaluated on all 3x3 submatrices of the response matrix (excluding the single agent row and column) and the minimum value is reported as LS 3x3 (originally suggested by Louis Staudt.
- **Beta**: The parameter that minimizes the difference between the observed combination effect and that obtained fom the Bliss independence model. Values less than 1, greater than 1 and equal to 1 indicate synergy, antagonism and non-interaction respectively. See Cokol et al for more details
- **Gamma**: The parameter that minimizes the difference between the observed combination effect and Gaddums non-interaction model. Values less than 1, greater than 1 and equal to 1 indicate synergy, antagonism and non-interaction respectively. See Cokol et al for more details
- **DBSumNeg**: The sum of the negative deviations from the Bliss model. In practice this is simply the sum of the negative elements of the ΔBliss matrix
- **DBSumPos**: The sum of the positive deviations from the Bliss model. In practice this is simply the sum of the positive elements of the ΔBliss matrix
- **Δ Bliss** - the excess over the Bliss model at each combination. More negative values indicate that the combination is better than the activity predictied by the Bliss model. A value of 0 indicates that the combination is no different from that predicted by the Bliss model

How to Add a New Assay

1. Login to the tripod site
2. Click the folder in the left panel that you want to add the new assay to
3. Click “New Assay” at the top of the page
4. Fill in information
5. Click “Create Assay”
6. Refresh browser and your new assay will appear

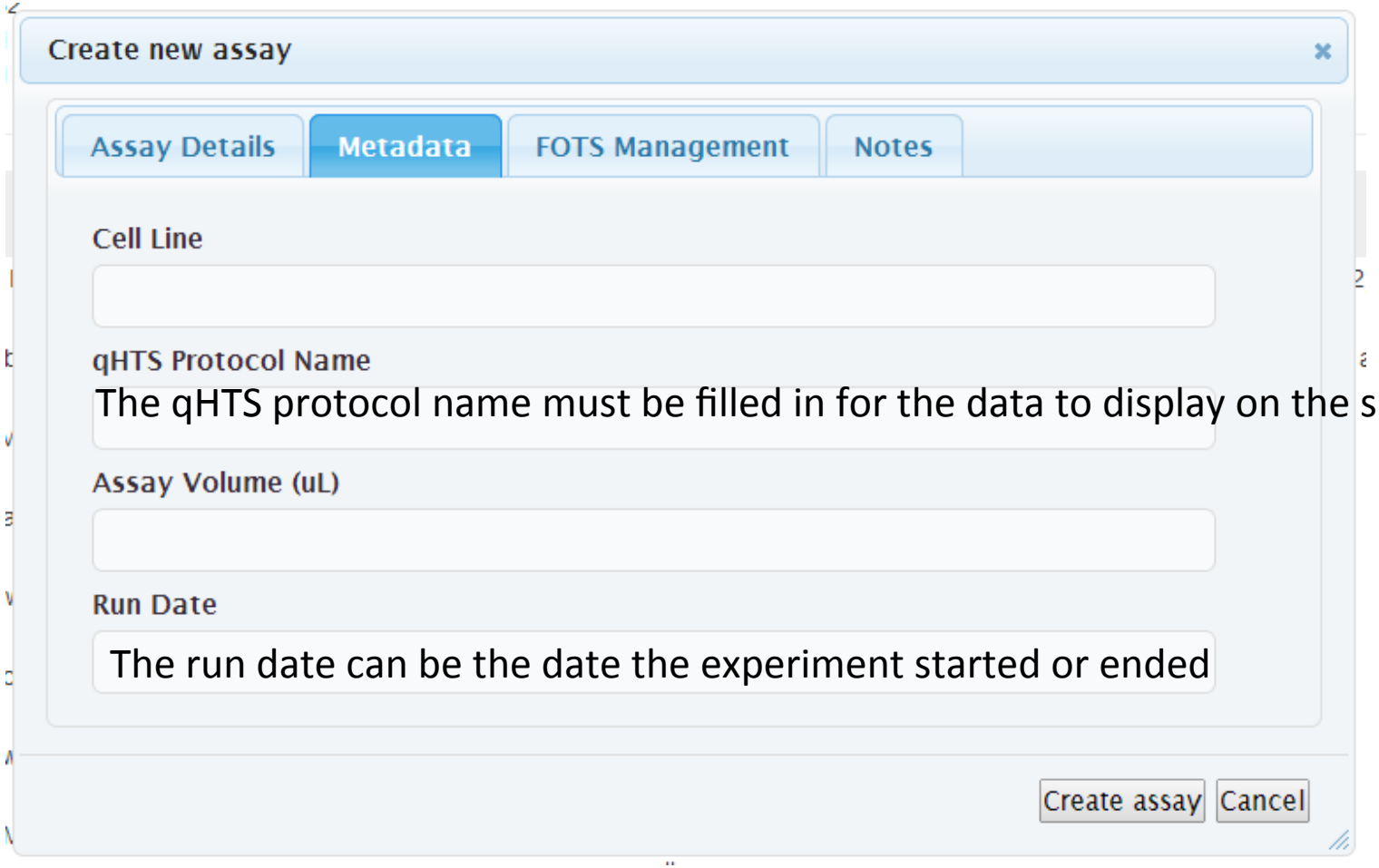

Combination Screening @
https://tripod.nih.gov/matrix-client/#new/assay
Matrix@NCATS
New Project
New Assay
Edit Project
Edit Assay
Compare selected assays
Help
Filter projects ...
ALK
ATAD5
ATL
BRAF Inhibitor Curve Shift
BX and PF Combination
Birinapant
Bladder Cancer
Brachyury_Lung Cancer
Braf Minigene
CD47
CLL
Cancer Stem Cells
DIPG
DLBCL
DNA repair combinations
Elesclomol
Ewings Sarcoma
Ewings Sarcoma/Guanine
Name
DLBCL
Louis Staudt
Start Date
12/01/2010
Notes
HBL1
TMD8
SUDHL2
U2932
RPMI + 10% FBS+P/S for growth
RPMI + 5% FBS-no phenol+P/S for screen
ID
Name
Type
No.
166
4x4s with Lou Staudt's Lines and Harold Varmus line
drug vs all
2
167
First 4x4 beta test for Lou Staudt
drug vs all
2

Fill in New Assay Details

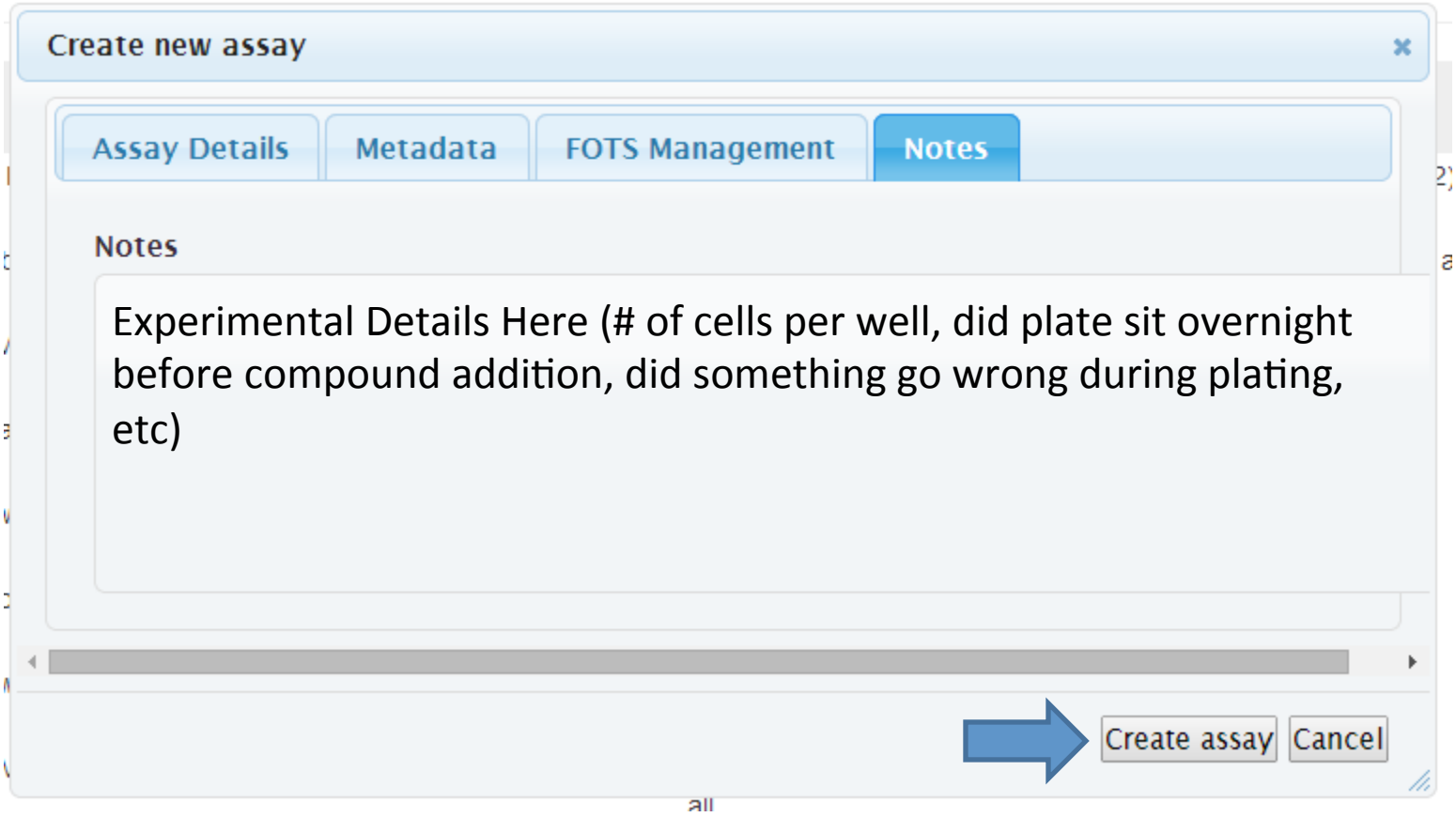


Choose Project from pull down menu
Select MIPE version from pull down menu

Fill in New Assay Details

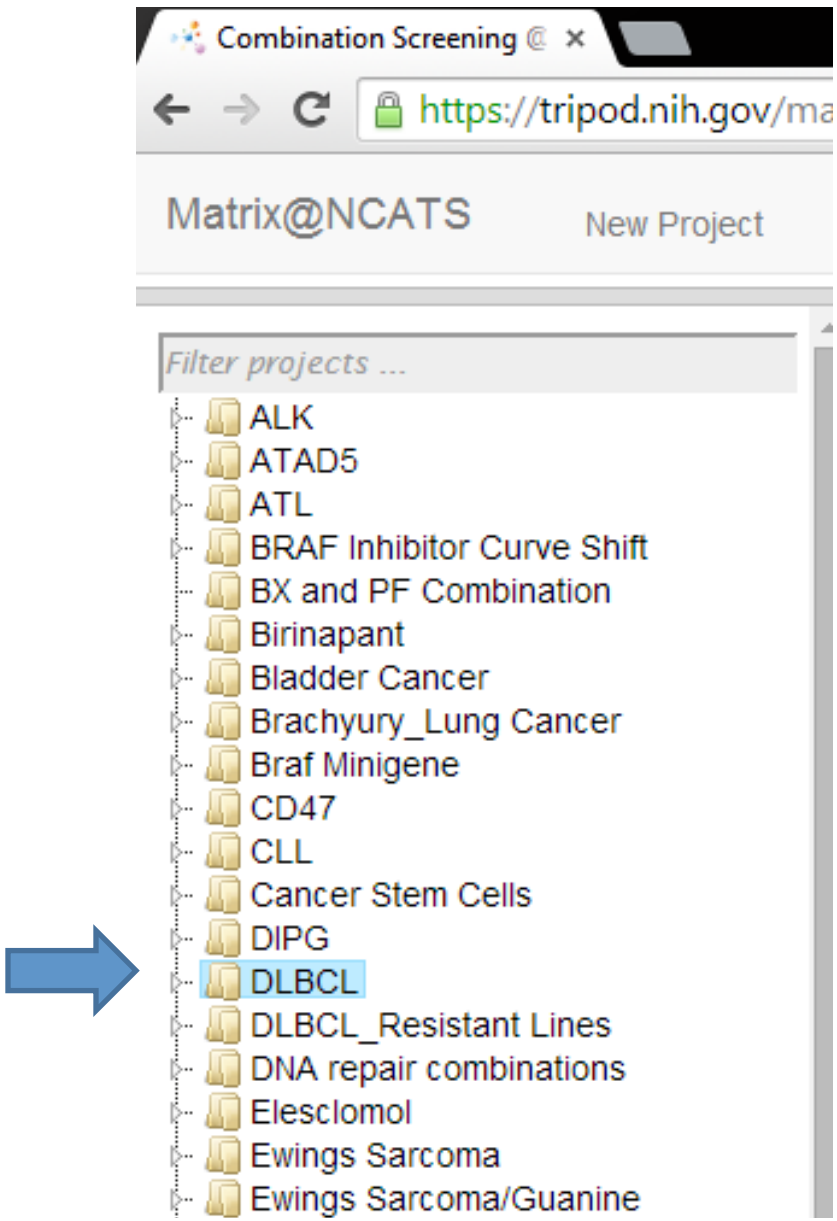


Fill in New Assay Details



How to Edit an Assay

1. Click the arrow by the folder in the left panel to display all assays
2. Click on the assay you want to edit
3. Click “Edit Assay” in the top left
4. Fill in information
5. Click “Save Changes”
6. Refresh browser and changes will appear


Combination Screening @
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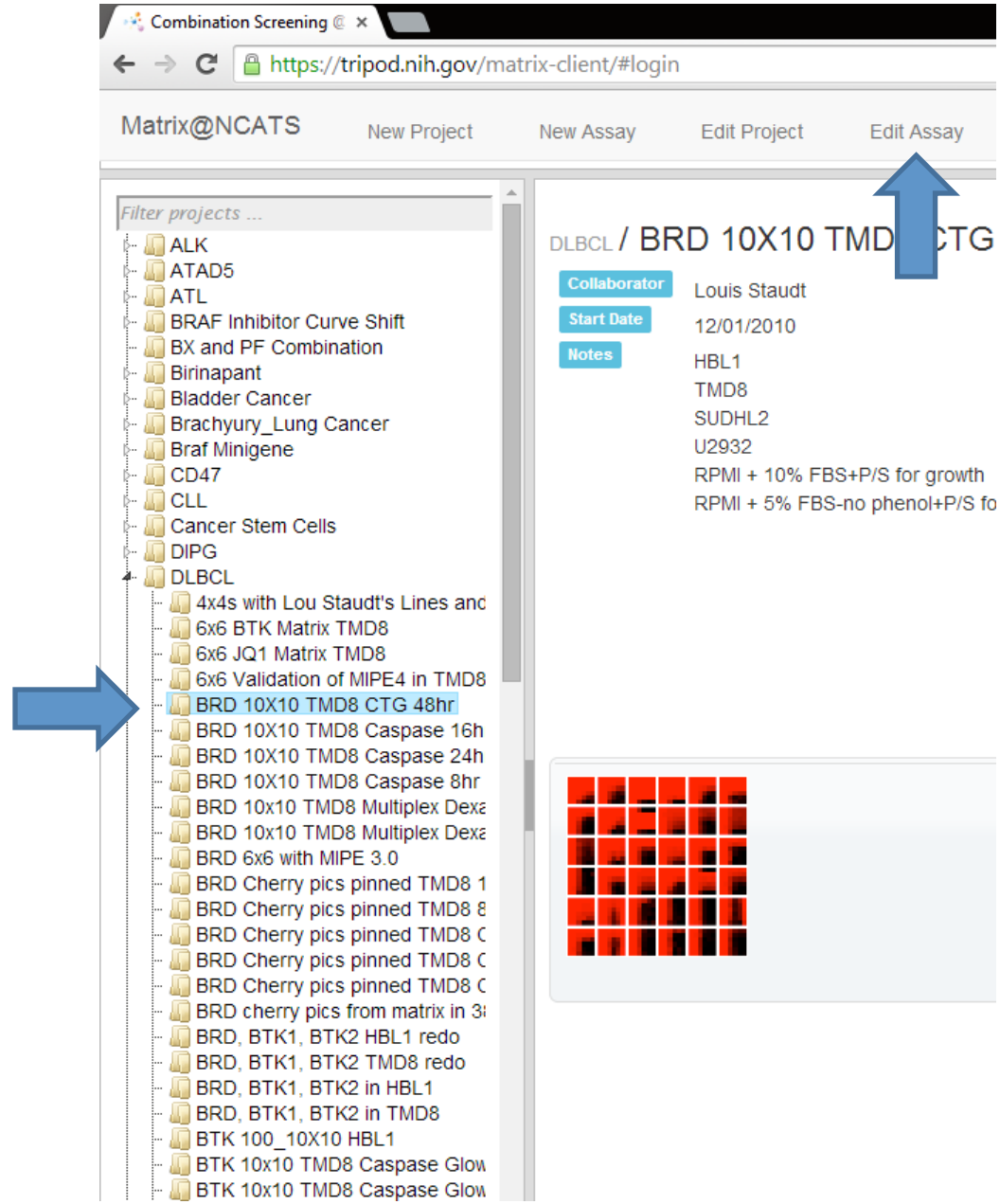
Matrix@NCATS
New Project
Filter projects ...
ALK
ATAD5
ATL
BRAF Inhibitor Curve Shift
BX and PF Combination
Birinapant
Bladder Cancer
Brachyury_Lung Cancer
Braf Minigene
CD47
CLL
Cancer Stem Cells
DIPG
DLBCL
DLBCL_Resistant Lines
DNA repair combinations
Elesclomol
Ewings Sarcoma
Ewings Sarcoma/Guanine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ALK
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BX and PF Combination
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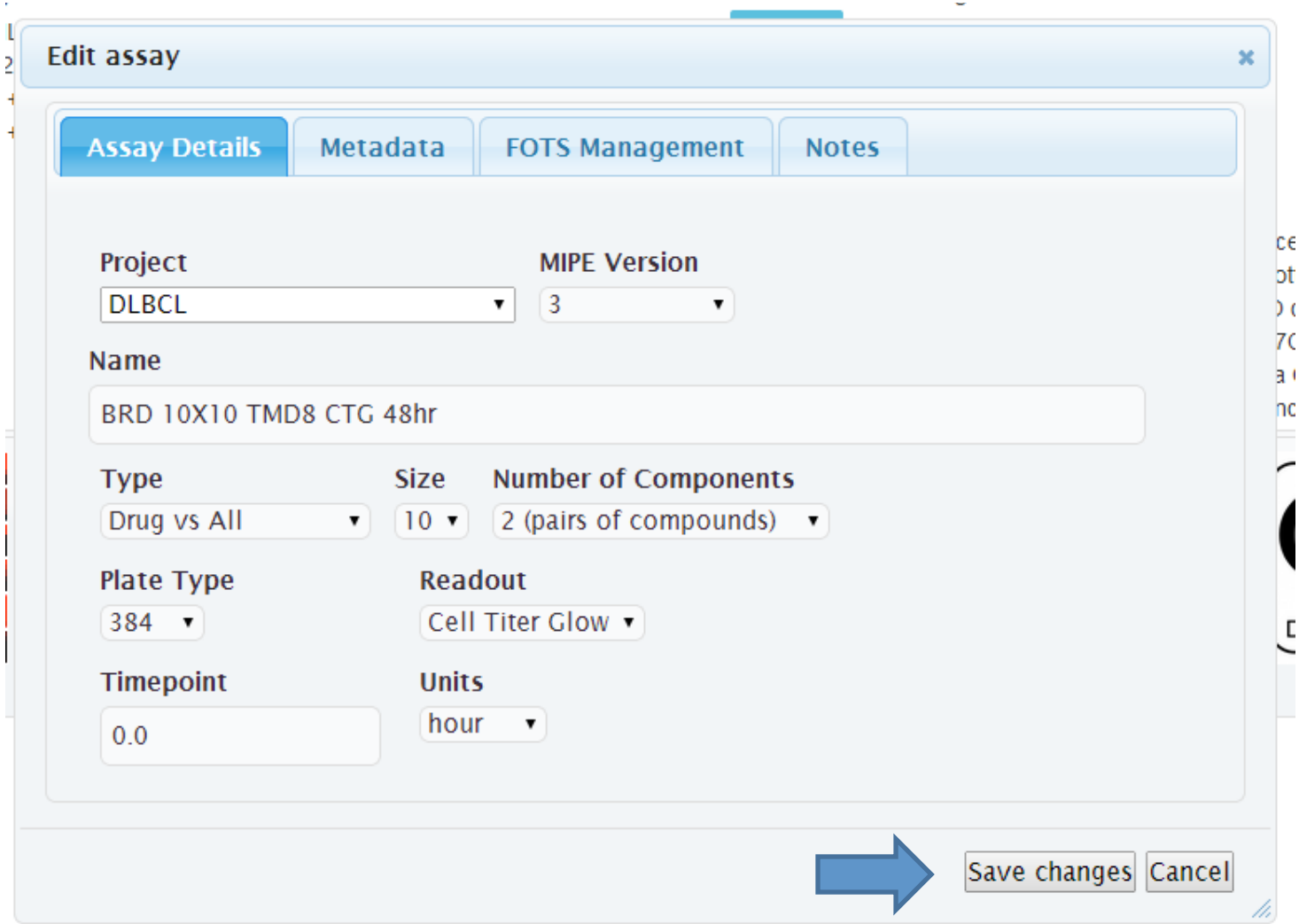
Bladder Cancer
Brachyury_Lung Cancer
Braf Minigene
CD47
CLL
Cancer Stem Cells
DIPG
DLBCL
4x4s with Lou Staudt's Lines and
6x6 BTK Matrix TMD8
6x6 JQ1 Matrix TMD8
6x6 Validation of MIPE4 in TMD8
BRD 10X10 TMD8 CTG 48hr
BRD 10X10 TMD8 Caspase 16h
BRD 10X10 TMD8 Caspase 24h
BRD 10X10 TMD8 Caspase 8hr
BRD 10x10 TMD8 Multiplex Dexa
BRD 10x10 TMD8 Multiplex Dexa
BRD 6x6 with MIPE 3.0
BRD Cherry pics pinned TMD8 1
BRD Cherry pics pinned TMD8 8
BRD Cherry pics pinned TMD8 C
BRD Cherry pics pinned TMD8 C
BRD Cherry pics pinned TMD8 C
BRD cherry pics from matrix in 3
BRD, BTK1, BTK2 HBL1 redo
BRD, BTK1, BTK2 TMD8 redo
BRD, BTK1, BTK2 in HBL1
BRD, BTK1, BTK2 in TMD8
BTK 100_10X10 HBL1
BTK 10x10 TMD8 Caspase Glow
BTK 10x10 TMD8 Caspase Glow
DLBCL / BRD 10X10 TMD CTG
Collaborator
Louis Staudt
Start Date
12/01/2010
Notes
HBL1
TMD8
SUDHL2
U2932
RPMI + 10% FBS+P/S for growth
RPMI + 5% FBS-no phenol+P/S fo

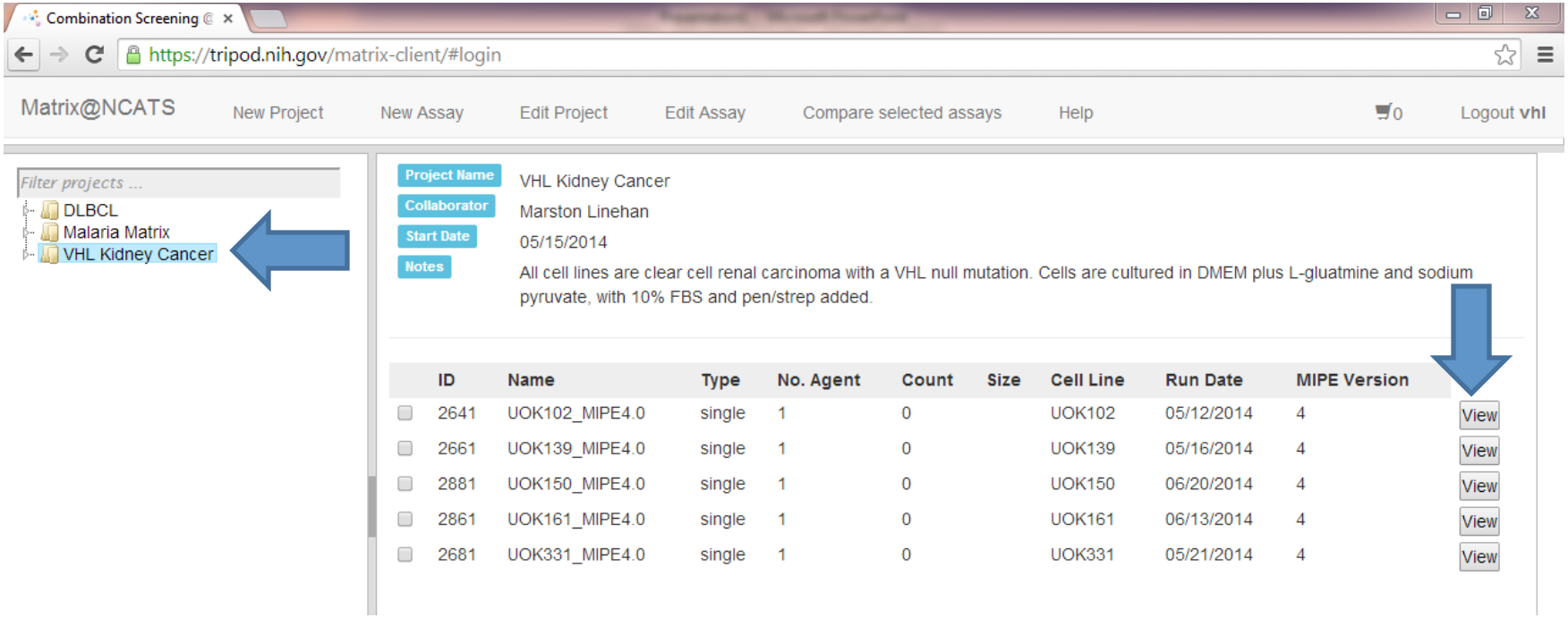
Edit Assay Details



Viewing and Downloading Data

1. Click on your Assay of interest in the left panel
2. Click the Heatmap Icon to view dose response curves (single agent screen) or matrix (combination screen)
3. Click the List Icon to view individual information for each compound or combination screened
4. Click the QC Diagnostics Icon for QC information on that assay

Viewing Data Online

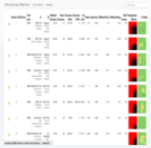


- Click on the VHL Kidney Cancer folder on the right panel
- Then click View on the far right

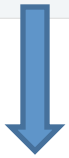
VHL Kidney Cancer / UOK102_MIPE4.0

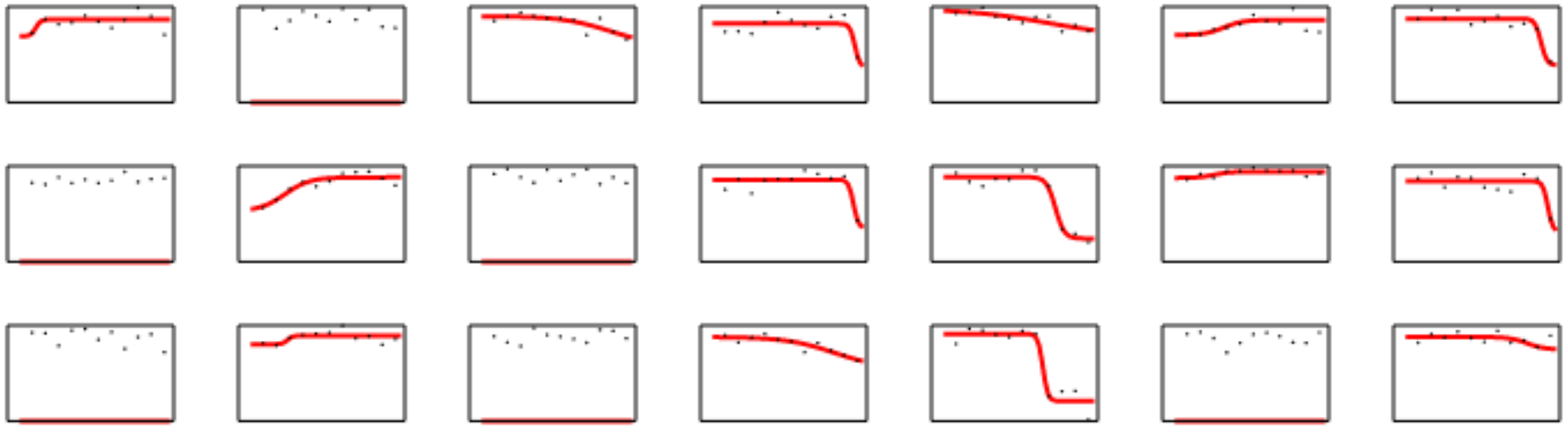
Collaborator	Marston Linehan
Start Date	05/15/2014
Notes	All cell lines are clear cell renal carcinoma with a VHL null mutation. Cells are cultured in DMEM plus L-gluatmine and sodium pyruvate, with 10% FBS and pen/strep added.

Assay ID	2641
Canonical Name	384_0x0_4_single_UOK102_Marston Linehan_Cell Titer Glow_48.0 hour
FOTS ID Type	single with MIPE v4
Num Component	1
Block Size qHTS protocol	s-vhl-UOK102-1
Assay Volume	5.0 uL
Readout	Cell Titer Glow at 48.0 hour
Run date	05/12/2014
Notes	UOK102 cells were plated at 500 cells per well then incubated for 4 hours. Next, compounds were added. Plates incubated with compound for 48 hours then Cell Titer Glo was added.



QC DIAGNOSTICS

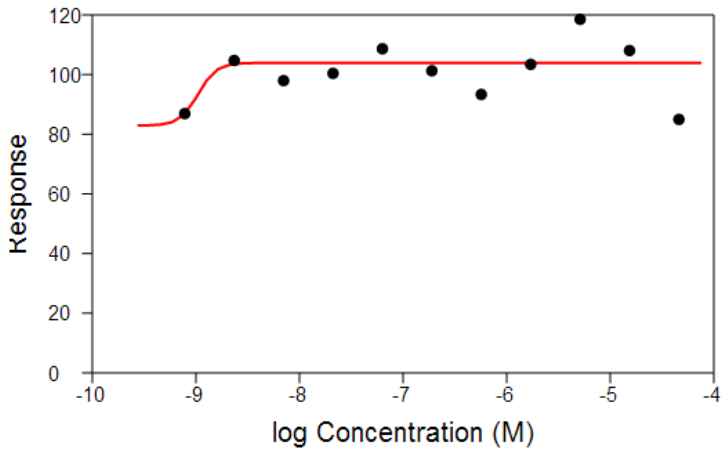




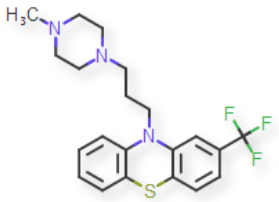
Serial	NCGC ID	Name	Target	MoA	AC50 (uM)	Hill Slope	Infinity	Zero	Curve Class[?]	Curve Class2[?]	Read
1	NCGC00013226-15	Trifluoperazine hydrochloride	DRD2	Nav1.4 (SkM1) Sodium Channel Blockers;Nav 1.7 (PN1/hNE-Na) Sodium Channel Blockers	0.00	4.95	103.90	82.90	1.3	1.4	ac ty

NCGC00013226-15 Trifluoperazine hydrochloride

activity



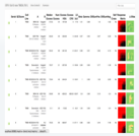
Curve class	1.3
Curve class 2	1.4
AC_{50}	0.00 uM
Hill slope	4.95
Zero Activity	82.90
Inf. Activity	103.90



NCGC ID	NCGC00013226-15
Name	Trifluoperazine hydrochloride
MoA	Nav1.4 (SkM1) Sodium Channel Blockers;Nav1.7 (PN1/hNE-Na) Sodium Channel Blockers
Aliases	Trifluoperazine dihydrochloride, Trifluoperazine Hcl, Stelabid, Stelazine, Stelazine trifluoperzine, Trifluoperazina
CAS RN	440-17-5
Alt. Mechanism	

VHL Kidney Cancer / UOK102_MIPE4.0

Collaborator	Marston Linehan
Start Date	05/15/2014
Notes	All cell lines are clear cell renal carcinoma with a VHL null mutation. Cells are cultured in DMEM plus L-gluatmine and sodium pyruvate, with 10% FBS and pen/strep added.
Assay ID	2641
Canonical Name	384_0x0_4_single_UOK102_Marston Linehan_Cell Titer Glow_48.0 hour
FOTS ID Type	single with MIPE v4
Num Component	1
Block Size qHTS protocol	s-vhl-UOK102-1
Assay Volume	5.0 uL
Readout	Cell Titer Glow at 48.0 hour
Run date	05/12/2014
Notes	UOK102 cells were plated at 500 cells per well then incubated for 4 hours. Next, compounds were added. Plates incubated with compound for 48 hours then Cell Titer Glo was added.



Only 10 compounds will display by default. To display everything, select all in the pull down menu then click the refresh button.

Download all data here!

1912 samples, 1 readout

Download data

Items to display 10

Highlight actives

← Previous

Next →

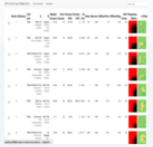
Clicking on any of the headings will sort all the data by that column

Serial	NCGC ID	Name	Target	MoA	AC50 (uM)	Hill Slope	Infinity	Zero	Curve Class?	Curve Class2?	Readout	
1	NCGC00013226-15	Trifluoperazine hydrochloride	DRD2	Nav1.4 (SkM1) Sodium Channel Blockers;Nav 1.7 (PN1/hNE-Na) Sodium Channel Blockers	0.00	4.95	103.90	82.90	1.3	1.4	activity	
2	NCGC00013724-01	Methscopolamine bromide		Muscarinic Antagonists	1000000.00	0.00	0.00	0.00	5	4	activity	

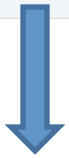
VHL Kidney Cancer / UOK102_MIPE4.0

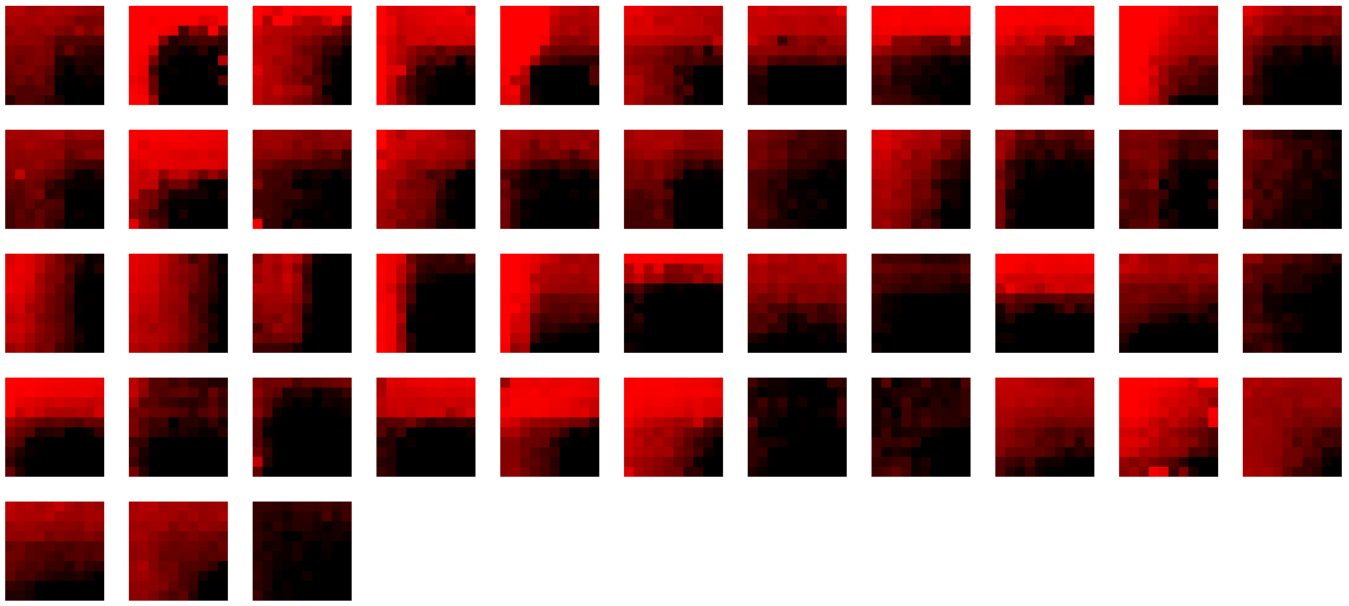
Collaborator	Marston Linehan
Start Date	05/15/2014
Notes	All cell lines are clear cell renal carcinoma with a VHL null mutation. Cells are cultured in DMEM plus L-gluatmine and sodium pyruvate, with 10% FBS and pen/strep added.

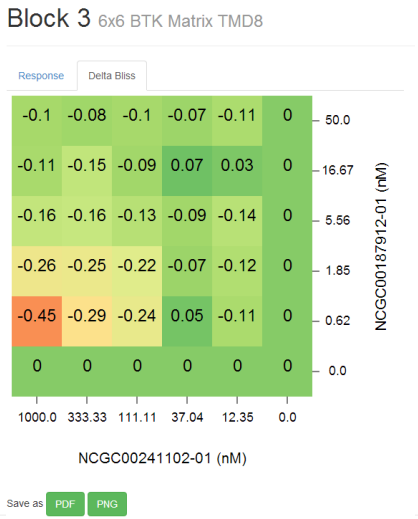
Assay ID	2641
Canonical Name	384_0x0_4_single_UOK102_Marston Linehan_Cell Titer Glow_48.0 hour
FOTS ID Type	single with MIPE v4
Num Component	1
Block Size qHTS protocol	s-vhl-UOK102-1
Assay Volume	5.0 uL
Readout	Cell Titer Glow at 48.0 hour
Run date	05/12/2014
Notes	UOK102 cells were plated at 500 cells per well then incubated for 4 hours. Next, compounds were added. Plates incubated with compound for 48 hours then Cell Titer Glo was added.



QC DIAGNOSTICS

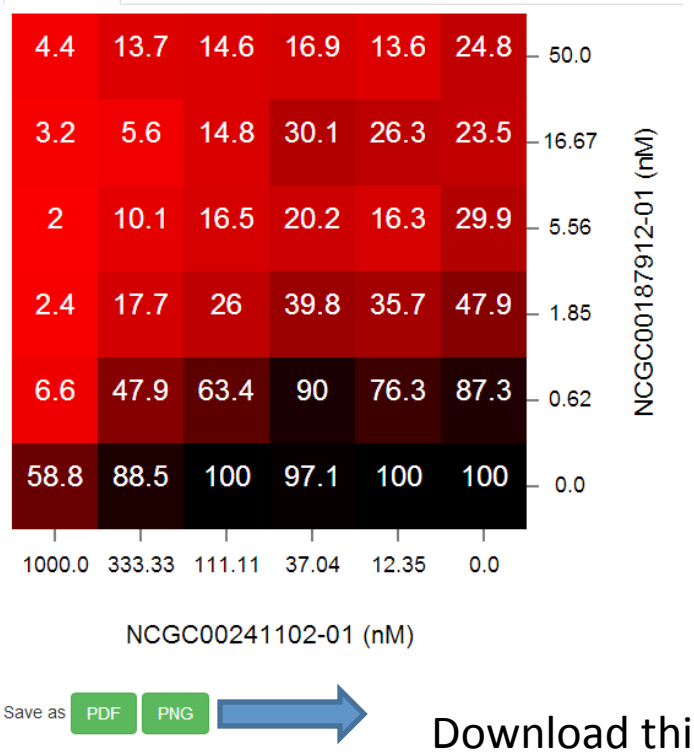


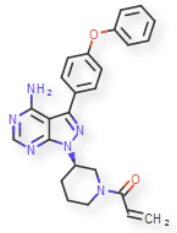




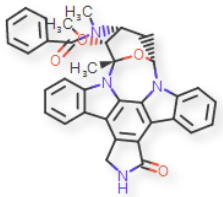
Red wells = viability readout, values are from CTG

Green wells = synergy assessment based on viability readout





NCGC ID	NCGC00187912-01
Name	PCI-32765
MoA	Btk/Lck/Lyn inhibitor
Aliases	PCI-32765
CAS RN	936563-96-1
Alt. Mechanism	
Phase	

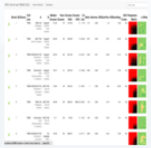


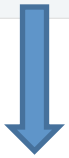
NCGC ID	NCGC00241102-01
Name	Midostaurin
MoA	PKC/flt3 inhibitor
Aliases	Midostaurin, PKC 412, CGP-41251/PKC-412
CAS RN	120685-11-2
Alt. Mechanism	
Phase	

Download this specific matrix data

VHL Kidney Cancer / UOK102_MIPE4.0

Collaborator	Marston Linehan
Start Date	05/15/2014
Notes	All cell lines are clear cell renal carcinoma with a VHL null mutation. Cells are cultured in DMEM plus L-gluatmine and sodium pyruvate, with 10% FBS and pen/strep added.
Assay ID	2641
Canonical Name	384_0x0_4_single_UOK102_Marston Linehan_Cell Titer Glow_48.0 hour
FOTS ID Type	single with MIPE v4
Num Component	1
Block Size qHTS protocol	s-vhl-UOK102-1
Assay Volume	5.0 uL
Readout	Cell Titer Glow at 48.0 hour
Run date	05/12/2014
Notes	UOK102 cells were plated at 500 cells per well then incubated for 4 hours. Next, compounds were added. Plates incubated with compound for 48 hours then Cell Titer Glo was added.





TMD8

https://tripod.nih.gov/matrix-client/rest/matrix/blocks/168/table

6x6 BTK Matrix TMD8 (168) Show ComboID Selection Download 0 Filter rows

	Serial	QCScore	Cell Line	A	B	Median Excess	Num Excess	Excess HSA	Excess CRX	LS 3x3	Beta	Gamma	DBSumPos	DBSumNeg	Self Cross	Response Matrix	Δ Bliss
	1		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Canertinib *EGFR (HER1; erbB1) inhibitor*	84.21	6	581.06	581.06	11.74	1.19	1.18	6.67	-0.55	No		
	2		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Neratinib *EGFR (HER1; erbB1) inhibitor*	78.45	18	-207.68	-207.68	-14.72	0.93	0.91	0.38	-1.86	No		
	3		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Midostaurin *PKC/flt3 inhibitor*	91.03	22	-424.84	-424.84	-27.91	0.87	0.83	0.15	-3.5	No		
	4		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	TAE-684 *Anaplastic Lymphoma Kinase (ALK) Inhibitor*	86.5	24	-282.82	-282.82	-13.49	0.9	0.89	0.03	-2.67	No		
	5		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	AZD-7762 *Chk1/2 Inhibitor*	90.19	14	-205.84	0	-17.56	0.9	0.85	0.17	-1.69	No		

TMD8

https://tripod.nih.gov/matrix-client/rest/matrix/blocks/168/table

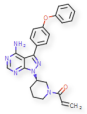
6x6 BTK Matrix TMD8 (168) Show ComboID Selection Download 0 Filter rows

	Serial	QCScore	Cell Line	A	B	Median Excess	Num Excess	Excess HSA	Excess CRX	LS 3x3	Beta	Gamma	DBSumPos	DBSumNeg	Self Cross	Response Matrix	Δ Bliss
	1		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Canertinib *EGFR (HER1; erbB1) inhibitor*	84.21	6	581.06	581.06	11.74	1.19	1.18	6.67	-0.55	No		
	2		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Neratinib *EGFR (HER1; erbB1) inhibitor*	78.45	18	-207.68	-207.68	-14.72	0.93	0.91	0.38	-1.86	No		
	3		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	Midostaurin *PKC/flt3 inhibitor*	91.03	22	-424.84	-424.84	-27.91	0.87	0.83	0.15	-3.5	No		
	4		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	TAE-684 *Anaplastic Lymphoma Kinase (ALK) Inhibitor*	86.5	24	-282.82	-282.82	-13.49	0.9	0.89	0.03	-2.67	No		
	5		TMD8	PCI-32765 *Btk/Lck/Lyn inhibitor*	AZD-7762 *Chk1/2 Inhibitor*	90.19	14	-205.84	0	-17.56	0.9	0.85	0.17	-1.69	No		

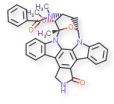
Block 3 6x6 BTK Matrix TMD8

Response Delta Bliss

NCGC00187912-01 (nM) \ NCGC00241102-01 (nM)	1000.0	333.33	111.11	37.04	12.35	0.0
50.0	4.4	13.7	14.6	16.9	13.6	24.8
16.67	3.2	5.6	14.8	30.1	26.3	23.5
5.56	2	10.1	16.5	20.2	16.3	29.9
1.85	2.4	17.7	26	39.8	35.7	47.9
0.62	6.6	47.9	63.4	90	76.3	87.3
0.0	58.8	88.5	100	97.1	100	100

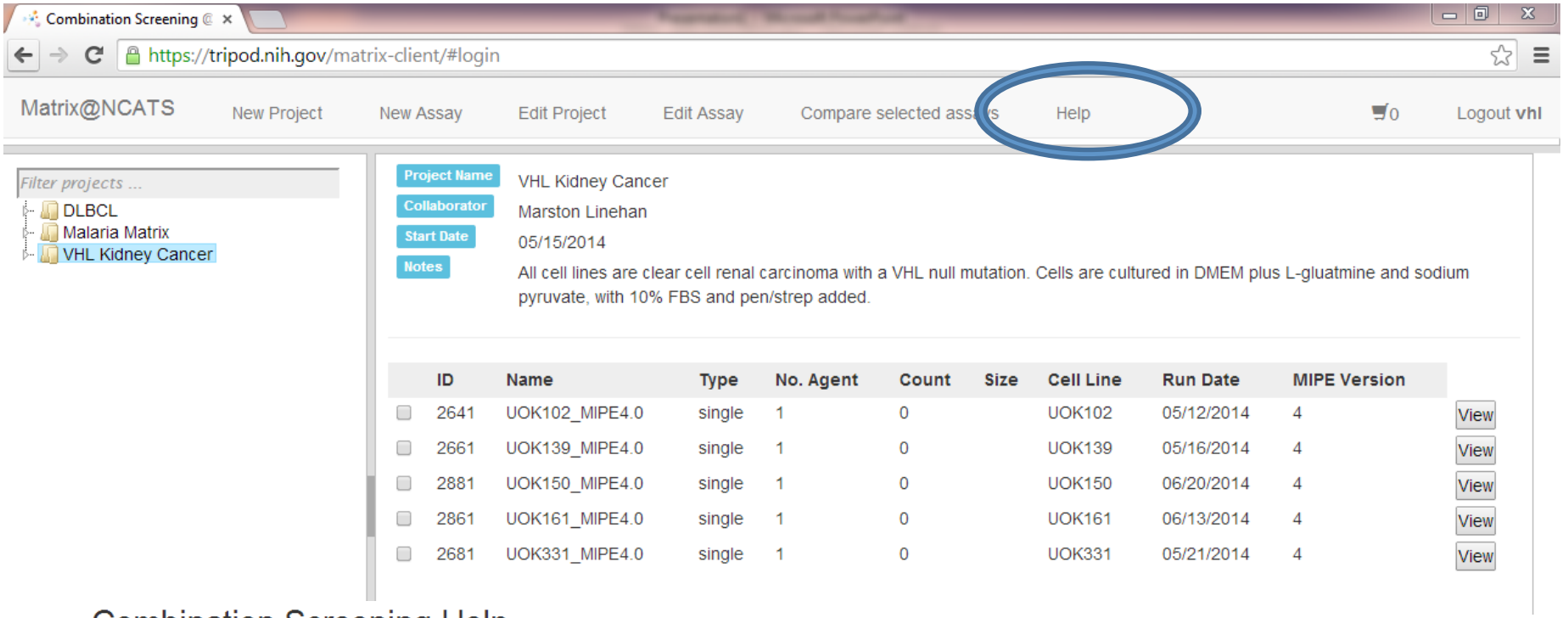


NCGC ID	NCGC00187912-01
Name	PCI-32765
MoA	Btk/Lck/Lyn inhibitor
Aliases	PCI-32765
CAS RN	936563-96-1
Alt. Mechanism	
Phase	



NCGC ID	NCGC00241102-01
Name	Midostaurin
MoA	PKC/flt3 inhibitor
Aliases	Midostaurin, PKC 412, CGP-41251/PKC-412
CAS RN	120685-11-2
Alt. Mechanism	
Phase	

Save as PDF PNG



Combination Screening Help

The *Tabular* tab summarizes the results of a combination screen. Several metrics of synergy are reported and their details are provided below. Our experience has shown that no single metric is effective in characterizing synergy over a large number of cases and that correlation between some of these metrics are relatively poor.

Clicking on NCGC ID's (columns **A** and **B**) will display an information box for the compounds. Clicking on the heatmaps will display a larger version of the heatmap along with the information boxes of the two compounds for that combination. Clicking on column headers will allow you to sort the entire table by that column.

- **MedianExcess**: The median of the sum of the differences between the combination responses and the single agent responses. More positive values are better
- **NumExcess**: The number of combinations in a block that show a better combination responses than *both* the corresponding single agents. Larger is better
- **Excess HSA**: The HSA (see below) model is computed and the differences between each combination in the block and the corresponding HSA value are summed. More negative values are better
- **ExcessCRX**: An extension of the 'Excess HSA' metric that takes into account dilution factors. These factors are based on the EC_{90} and EC_{10} values of the single agent curves. Since the single agent curves are derived from the individual blocks, they can be noisy and thus the EC_{90} and EC_{10} can be inaccurate, resulting in noisy values for this metric. See Lehar et al for more information
- **LS 3x3**: The sum of the deviations from the HSA model are evaluated on all 3x3 submatrices of the response matrix (excluding the single agent row and column) and the minimum value is reported as LS 3x3 (originally suggested by Louis Staudt.
- **Beta**: The parameter that minimizes the difference between the observed combination effect and that obtained fom the Bliss independence model. Values less than 1, greater than 1 and equal to 1 indicate synergy, antagonism and non-interaction respectively. See Cokol et al for more details
- **Gamma**: The parameter that minimizes the difference between the observed combination effect and Gaddums non-interaction model. Values less than 1, greater than 1 and equal to 1 indicate synergy, antagonism and non-interaction respectively. See Cokol et al for more details
- **DBSumNeg**: The sum of the negative deviations from the Bliss model. In practice this is simply the sum of the negative elements of the ΔBliss matrix
- **DBSumPos**: The sum of the positive deviations from the Bliss model. In practice this is simply the sum of the positive elements of the ΔBliss matrix
- **Δ Bliss** - the excess over the Bliss model at each combination. More negative values indicate that the combination is better than the activity predictied by the Bliss model. A value of 0 indicates that the combination is no different from that predicted by the Bliss model

Support

- If you are having issues with the site itself (login problems, misssing projects, etc), please contact Raj Guha at guhar@mail.nih.gov